

TTTATTAAAAAGGTGACAAATCTCTATCAATTCTCAGGACCTTCCTGAAGGAACTACCAATAT 630
 Leu Leu Lys Lys Val Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr

AAAGTGGCTTTAAATGATAGCTGGAATAATCCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTG 700
 Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro Ser Asp Asn Ile Asn Leu Thr Val Pro

CCGGCGGTGCACACGTCACCTTTTTTCGTATATTCCGTCCACTCATGCAGTCTATGACACAATTAATAATCC 770
 Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro

TAATGCGGATTTACAAGTAGAAAGCGGGGTAAAACGGATCTCGTGACGGTTACTCTAGGGGAAGATCCA 840
 Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu Gly Glu Asp Pro

GATGTGAGCCATACTCTGTCCATTCAAACAGATGGCTATCAGGCAAAGCAGGTGATACCTCGTAATGTGC 910
 Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val

TTAATTCATCACAGTACTACTATTTCAGGAGATGATCTTGGGAATACCTATACACAGAAAGCAACAACCTT 980
 Leu Asn Ser Ser Gln³⁰⁹ Tyr^Y Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala Thr Thr Phe

TAAAGTCTGGGCACCAACTTCTACTCAAGTAAATGTTCTTCTTTATGACAGTGCAACGGGTCTGTAAACA 1050
 VWAP
 Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr

AAAATCGTACCTATGACGGCATCGGGCCATGGTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATT 1120
 Lys Ile Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu Asn

FIGURE 1B

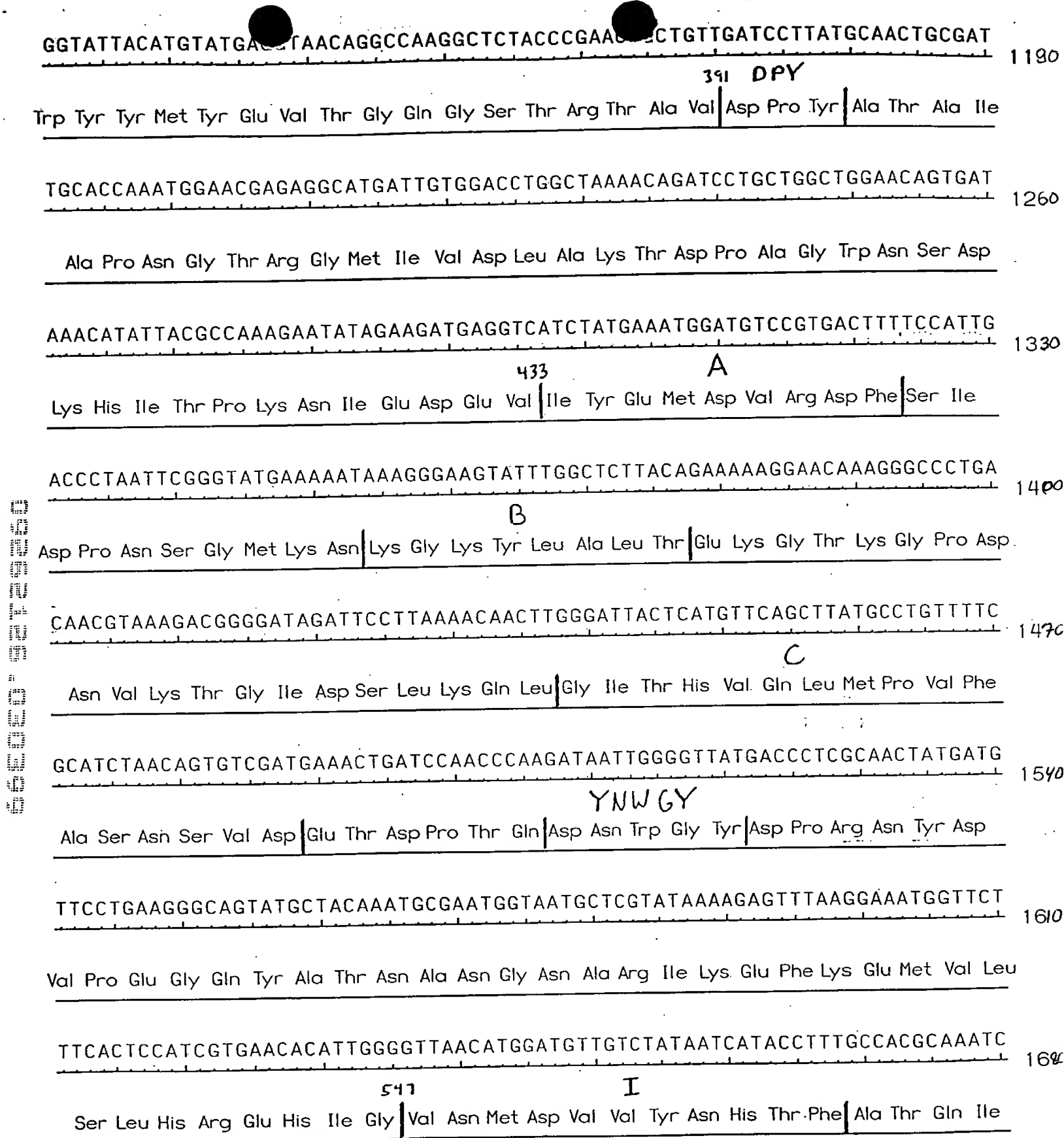


FIGURE 1C

TCTGACTTCGATAAA GTACCAGAATATTATTACCGTACGATGATCCAGGTAATTATACCAACGGATC

D

Ser Asp Phe Asp Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile Pro Thr Asp

AGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTTATTATTGATTCCCTTAAGTA

Gln Val Leu Glu Met Lys Leu ??? Ala Glu Arg Pro Met Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr

TTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGACTTAATGGCGCTGCTTGGAAAAGACACGATG

II

Trp Val Asn Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp Thr Met

TCCAAAGCTGCCTCGGAGCTTCATGCTATTAATCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTG

III

Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile Ala Leu Tyr Gly Glu Pro Trp Thr Gly

GAACCTCTGCACTGCCAGATGATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTT

Gly Thr Ser Ala Leu Pro Asp Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val Phe

TAATGACAATTTACGAAACGCGTTGGACGGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT

Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser Ser Ala Gln Gly Phe Ala Thr Gly

GCAACAGGCTTAAGTATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACTTTACCTCTTCACCAG

Ala Thr Gly Leu Thr Asp Ala Ile Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro

GTGAGACAATTAAGTATGTCACAAGTCATGATAACTACACCCTTTGGGACAAAATAGCCCTAAGCAATCC

IV

Gly Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp Lys Ile Ala Leu Ser Asn Pro

FIGURE 1D

TAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTCGCACAAAGCAGTTGTTATGACCTCACAAGGC	2310
Asn Asp Ser Glu Ala Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly	
GTTCCATTTCATGCAAGGCGGGGAAGAAATGCTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAG	2380
Val Pro Phe Met Gln Gly Gly Glu Glu Met Leu Arg ??? Lys Gly Gly Asn Asp Asn Ser Tyr Asn Ala	
GCGATGCGGTCAATGAGTTTGATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGG	2450
Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly	
GCTAATCCACCTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC	2520
Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile Asn Ser His Leu	
CAATTCCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAAGTATCATGTTAATAAAGACAAATGGG	2590
Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp	
GAAATATCATTGTTGTTTATAACCCAAATAAACTGTAGCAACCATCAATTTGCCGAGCGGGAAATGGGC	2660
Gly Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly Lys Trp Ala	
AATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCTTGGTCAAGCAGAGGGAAGTGTCCAAGTACCA	2730
Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu Gly Gln Ala Glu Gly Ser Val Gln Val Pro	
GGTATATCTATGATGATCCTTCATCAAGAGGTAAGCCCAGACCACGGTAAAAAGTAATAGAAAA	2794
Gly Ile Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys	

FIGURE 1E

118
108
30
158
145
34
198
177
54
233
209
54
273
244
72

	M X X X X X X X X X X X X X L V L X X X F X X X G X S X X X X G N X X T - - - - Y	Majority
	10 20 30 40	
1	M A K K L I Y V C L S V C L V L T W A F N V K G Q S A H A D G N T T T I I V H Y	pullseqsig.seq.PRO
1	M L R Y T R N A L V L G S L V L L S G C D - N G S S S S S S G N P D T - - - -	klebpnseqsig.seq.p
1	M - - - - - - - - - - V S I R R S F E A - - - - - - - - - - Y	subpull.seq.pro
	- - - - X D X Q X X X X X X - P X X X X X X E X X - - X X X X X X X V X X X D	Majority
	50 60 70 80	
41	F C P A G D Y Q P W S L W M W P K D G G G A E Y D F N Q P A D S F G A V A S A D	pullseqsig.seq.PRO
35	- - - - P D N Q D V V V R L - P D V A V P G E A V - - T A V E N Q A V I H L V D	klebpnseqsig.seq.p
12	- V D D M N	subpull.seq.pro
	I X G X X S X X X X X X X X X X X X - - - W X K E X X X X X X X X X X X N X V X X	Majority
	90 100 110 120	
81	I P G N P S Q V G I I V R T Q D - - - W T K D V S A D R Y I D L S K G N E V W L	pullseqsig.seq.PRO
68	I A G I T S S S A A D Y S S K N L Y L W N N E T C D A L S A P V A D W N D V S T	klebpnseqsig.seq.p
17	I - - - - - I T V L I P A E Q - - - - - K E I - - - - - - - - - -	subpull.seq.pro
	X X X X S X L X X X X X P	Majority
	130 140 150 160	
118	V E G N S Q I F Y N E K D A E D A A K P A V S N A Y L D A S N Q V L V K L S Q P	pullseqsig.seq.PRO
108	T P S G S D K Y G P Y W V I P L N K E S G C I N V I V R D G T D K L I D S - - -	klebpnseqsig.seq.p
30	- M T P P	subpull.seq.pro
	X X L X X X X X D F T - - - - - X X X X P V X X X X X X S L X X X X X X X X	Majority
	170 180 190 200	
158	L T L G E G X S G F T V H D D T A N K D I P V T S V K D A S L G Q D V T A V L A	pullseqsig.seq.PRO
145	- D L R V A F G D F T - - - - - D R T V S V - I A G N S A V Y D S R A D A F R	klebpnseqsig.seq.p
34	F R L E T E I T D F - - - - - P L A V R E E Y S L - - - - -	subpull.seq.pro
	X X F X X X X X X X X W X - - X X X T L L - - - - - X K X X X X L Y - - - - -	Majority
	210 220 230 240	
198	G T F Q H I F G G S D W A P D N H S T L L - - - - - K K V T N N L Y Q F S G D L	pullseqsig.seq.PRO
177	A A F G V A L A E A H W V - - D K N T L L W P G G Q D K P I V R L Y - - - - -	klebpnseqsig.seq.p
54	- -	subpull.seq.pro
	- E X X Y X Y X X X X X X X - X X X X X X X X X X L T V X X X X X V T F X X	Majority
	250 260 270 280	
233	P E G N Y Q Y K V A L N D S W N N P S Y P S D N I N L T V P A G G A H V T F S Y	pullseqsig.seq.PRO
209	- - - - Y S H S S K V A A D - G E G K F T D R Y L K L T P T T V S Q Q V S M R F	klebpnseqsig.seq.p
54	- E A K Y K Y - - - - - - - - - - - - - - - - V C V S D H P V T F G K	subpull.seq.pro
	I H X X X A X Y X X X X X P X - X X X V X S G X K T D L V X X A X X E D X X X X	Majority
	290 300 310 320	
273	I P S T H A V Y D T I N N P N A D L Q V E S G V K T D L V T V T L G E D P D V S	pullseqsig.seq.PRO
244	P H - - L S S Y A A F K L P D - N A N V D E L L Q G E T V A I A A A E D G I L I	klebpnseqsig.seq.p
72	I H C V R A - - - - - - - - - - S S G H K T D L Q I G A V - - - - -	subpull.seq.pro

FIGURE 2A

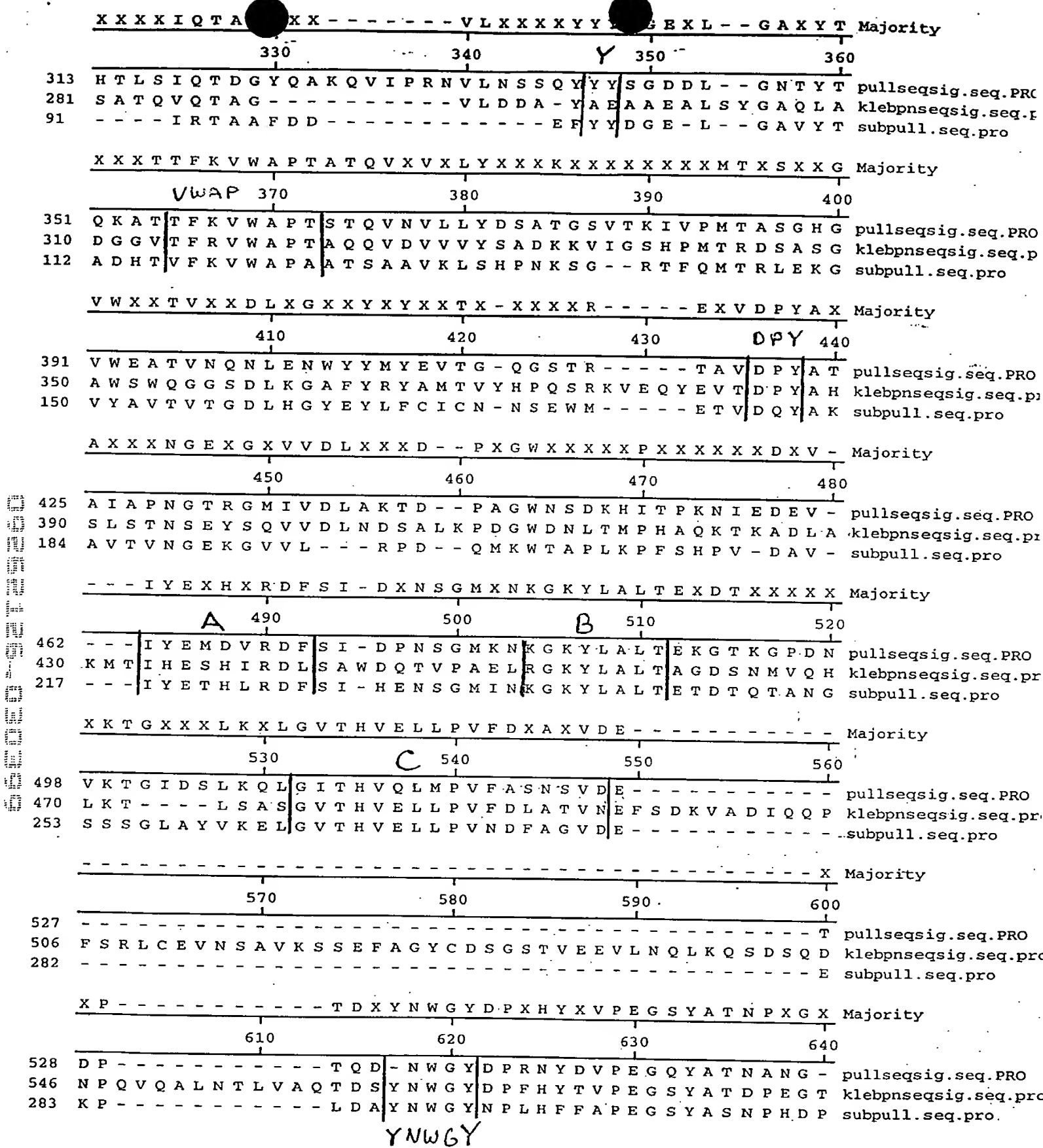


FIGURE 2B

X T R I K E F K X X X L H Q X - G X X V I M D V V Y T X A X X X S D - - Majority

650 660 670 680

555 N A R I K E F K E M V L S L H R E - H I G V N M D V V Y N H T F A T Q I S D - - pullseqsig.seq.PRO
586 - T R I K E F R T M I Q A I K Q D L G M N V I M D V V Y N H T N A A G P T D R T klebpnseqsig.seq.pr
312 Q T R K T E L K Q M I N T L H Q H - G L R V I L D V V F N H V Y K R E N S P - - subpull.seq.pro

- - F D K I V P X Y Y X R X X E X X X X X X X X X X D X A X E R R M X X K F Majority

690 700 710 720

592 - - F D K I V P E Y Y Y R T M I Q V I I P T D Q V L E M K L X A E R P M V Q K F pullseqsig.seq.PRO
625 S V L D K I V P W Y Y Q R L N E T T G S V E S A T C C S D S A P E H R M F A K L klebpnseqsig.seq.pr
349 - - F E K T V P G Y F F R H D E C G M P S N G T G V G N D I A S E R R M A R K F subpull.seq.pro

I A D S L X Y W X X E Y X I D G F R F D L M G X L X K D T X L X A X E X X X A X Majority

730 740 750 760

630 I I D S L K Y W V N E Y H I D G F R F D L M A L L G K D T M S K A A S E L H A I pullseqsig.seq.PRO
665 I A D S L A V W T T D Y K I D G F R F D L M G Y H P K A Q I L S A W E R I K A L klebpnseqsig.seq.pr
387 I A D C V V Y W L E E Y N V D G F R F D L L G I L D I D T V L Y M K E K A T K A subpull.seq.pro

N P G I X L F G E G W D X X T S X X X E X X X A X X A X K G X G I G X F N D X Majority

770 780 790 800

670 N P G I A L Y G E P W T G G T S A L P D D Q L L T K G A Q K G M G V A V F N D N pullseqsig.seq.PRO
705 N P D I Y F F G E G W D S N Q S D R F E - - I A S Q I N L K G T G I G T F S D R klebpnseqsig.seq.pr
427 K P G I L L F G E G W D L A T P L P H E Q K A A L A N A P R M P G I G F F N D M subpull.seq.pro

L R D A V X G N X - F D S X A - - - - Q G F A X G A G X L X X A X - - - - Majority

810 820 830 840

710 L R N A L D G N V - F D S S A - - - - Q G F A T G A T G L T D A I - - - - pullseqsig.seq.PRO
743 L R D S V R G G G P F D S G D A L R Q N Q G I G S G A G V L P N E L A S L S D D klebpnseqsig.seq.pr
467 F R D A V K G N T - F H L K A - - - - T G F A L G N G E S A Q A V - - - - subpull.seq.pro

- - - - - X X G X A G S - - - - - X X X K - - - - - A Majority

850 860 870 880

738 - - - - - K N G V E G S - - - - - pullseqsig.seq.PRO
783 Q V R H L A D L T R L G M A G N L A D F V M I D K D G A A K K G S E I D Y N G A klebpnseqsig.seq.pr
495 - - - - - M H G I A G S - - - - - S G W K - - - - - A subpull.seq.pro

X X X X X X X P X E X I N Y V X S H D N X T L W D K I S X X X P Q E X D - A X R Majority

890 900 910 920

745 I N D F T S S P G E T I N Y V T S H D N Y T L W D K I A L S N P N D S E - A D R pullseqsig.seq.PRO
823 P G G Y A A D P T E V V N Y V S K H D N Q T L W D M I S Y K A S Q E A D L A T R klebpnseqsig.seq.pr
507 L A P I V P E P S Q S I N Y V E S H D N H T F W D K M S F A L P Q E N D - S R K subpull.seq.pro

X X M Q X L A X A X V M L X Q G V P F X Q X G X E X L R X K X G X X N S Y X S G Majority

930 940 950 960

784 I K M D E L A Q A V V M T S Q G V P F M Q G G E E M L R X K G G N D N S Y N A G pullseqsig.seq.PRO
863 V R M Q A V S L A T V M L G Q G I A F D Q Q G S E L L R S K S F T R D S Y D S G klebpnseqsig.seq.pr
546 R S R Q R L A V A I I L L A Q G V P F I H S G Q E F F R T K Q G V E N S Y Q S S subpull.seq.pro

FIGURE 2C

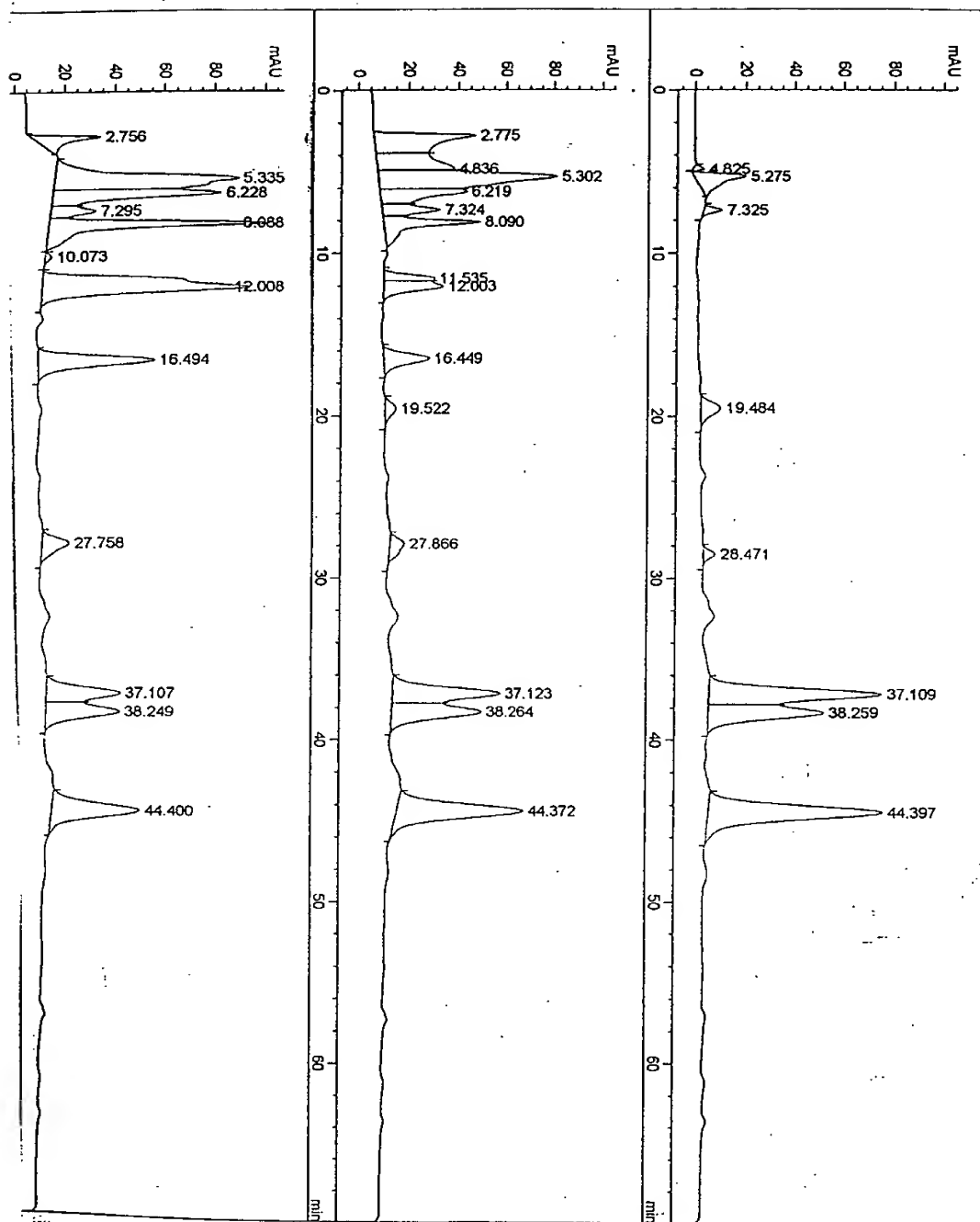


FIGURE 4 A, 4 B, 4 C

4 C

4 B

4 A

Percent Maximum Glucose Yield

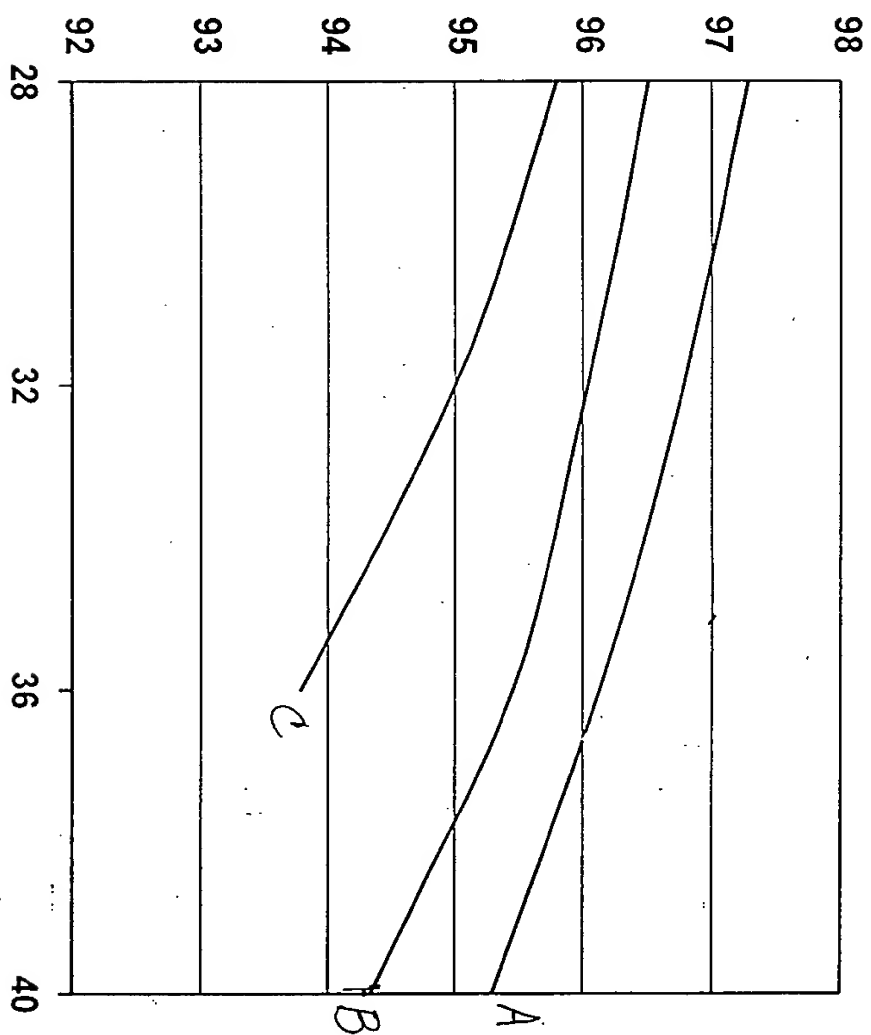


FIGURE 6

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	